

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 00:21:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6432728.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6432728 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6432728_1.fastq.gz SRR6432728_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 00:21:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6432728.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	432,803,854
Mapped reads	432,627,531 / 99.96%
Unmapped reads	176,323 / 0.04%
Mapped paired reads	432,627,531 / 99.96%
Mapped reads, first in pair	216,319,213 / 49.98%
Mapped reads, second in pair	216,308,318 / 49.98%
Mapped reads, both in pair	432,564,652 / 99.94%
Mapped reads, singletons	62,879 / 0.01%
Secondary alignments	0
Supplementary alignments	187,764 / 0.04%
Read min/max/mean length	30 / 150 / 139.81
Duplicated reads (estimated)	215,322,073 / 49.75%
Duplication rate	33%
Clipped reads	116,621,553 / 26.95%

2.2. ACGT Content

Number/percentage of A's	16,274,162,151 / 27.43%
Number/percentage of C's	12,783,654,048 / 21.55%
Number/percentage of T's	16,055,035,745 / 27.06%
Number/percentage of G's	14,212,262,602 / 23.96%
Number/percentage of N's	301,781 / 0%

GC Percentage	45.5%
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2.3. Coverage

Mean	19.1824
Standard Deviation	54.0749

2.4. Mapping Quality

Mean Mapping Quality	55.44
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2.5. Insert size

Mean	52,994
Standard Deviation	2,326,169.84
P25/Median/P75	290 / 307 / 323

2.6. Mismatches and indels

General error rate	0.98%
Mismatches	562,154,040
Insertions	12,091,914
Mapped reads with at least one insertion	2.73%
Deletions	39,408,925
Mapped reads with at least one deletion	8.7%
Homopolymer indels	51.56%

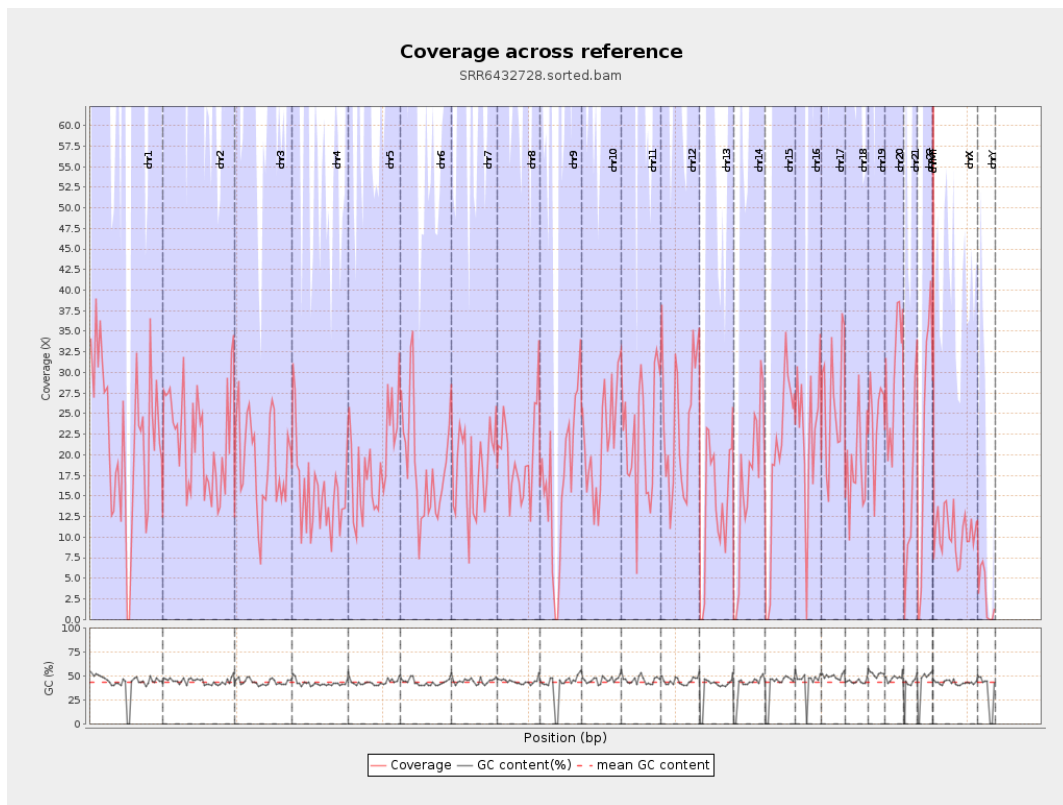
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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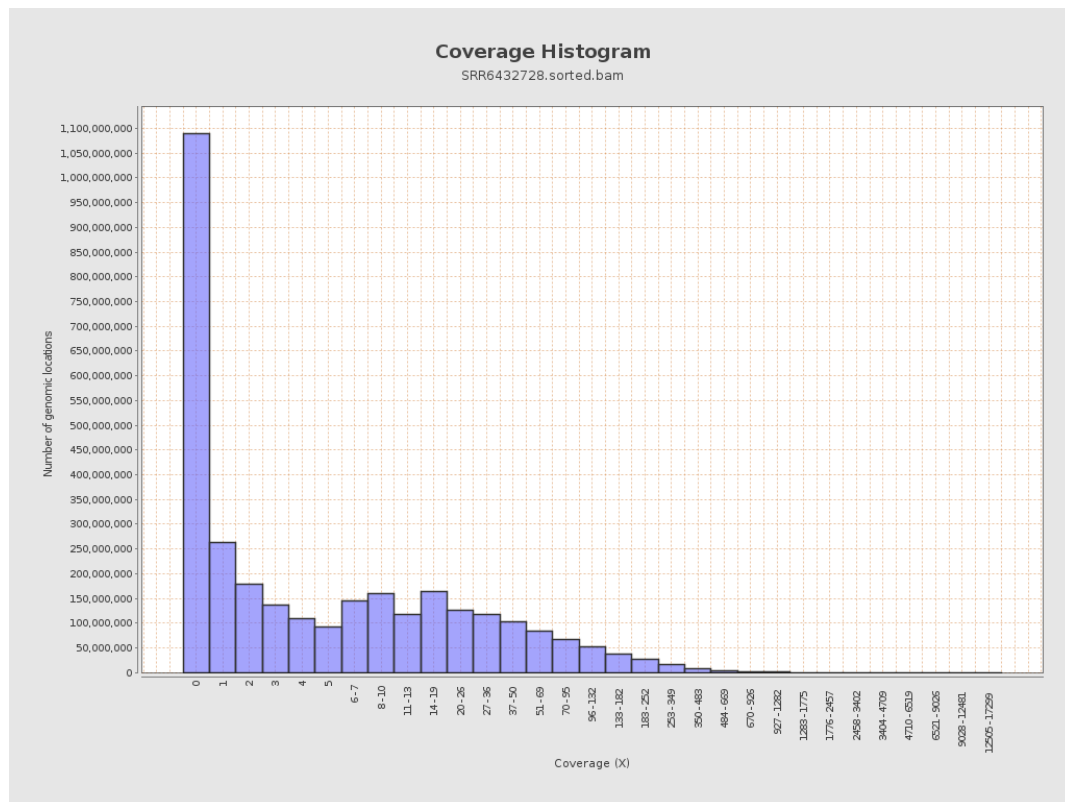
		bases	coverage	deviation
chr1	249250621	5455865631	21.8891	60.6719
chr2	243199373	5303246502	21.8062	62.0711
chr3	198022430	3754802692	18.9615	49.3608
chr4	191154276	2946595400	15.4148	44.0984
chr5	180915260	3456342781	19.1048	51.4218
chr6	171115067	3138304968	18.3403	49.6686
chr7	159138663	2928847321	18.4044	48.9429
chr8	146364022	2909112170	19.8759	52.1299
chr9	141213431	2385665086	16.894	54.2388
chr10	135534747	2921864961	21.5581	55.8377
chr11	135006516	2996358881	22.1942	56.9061
chr12	133851895	3204365813	23.9396	62.2214
chr13	115169878	1587485148	13.7839	41.7915
chr14	107349540	1784837486	16.6264	47.7244
chr15	102531392	1994515391	19.4527	55.3633
chr16	90354753	2063085832	22.8332	65.1595
chr17	81195210	2139120340	26.3454	66.6047
chr18	78077248	1424354475	18.2429	51.8251
chr19	59128983	1443986980	24.421	65.1865
chr20	63025520	1855651709	29.4429	71.1011
chr21	48129895	723906579	15.0407	53.287
chr22	51304566	1146446095	22.3459	64.5001
chrMT	16571	5465542	329.8257	611.7483
chrX	155270560	1635009721	10.5301	30.1246

chrY	59373566	177617517	2.9915	22.4605
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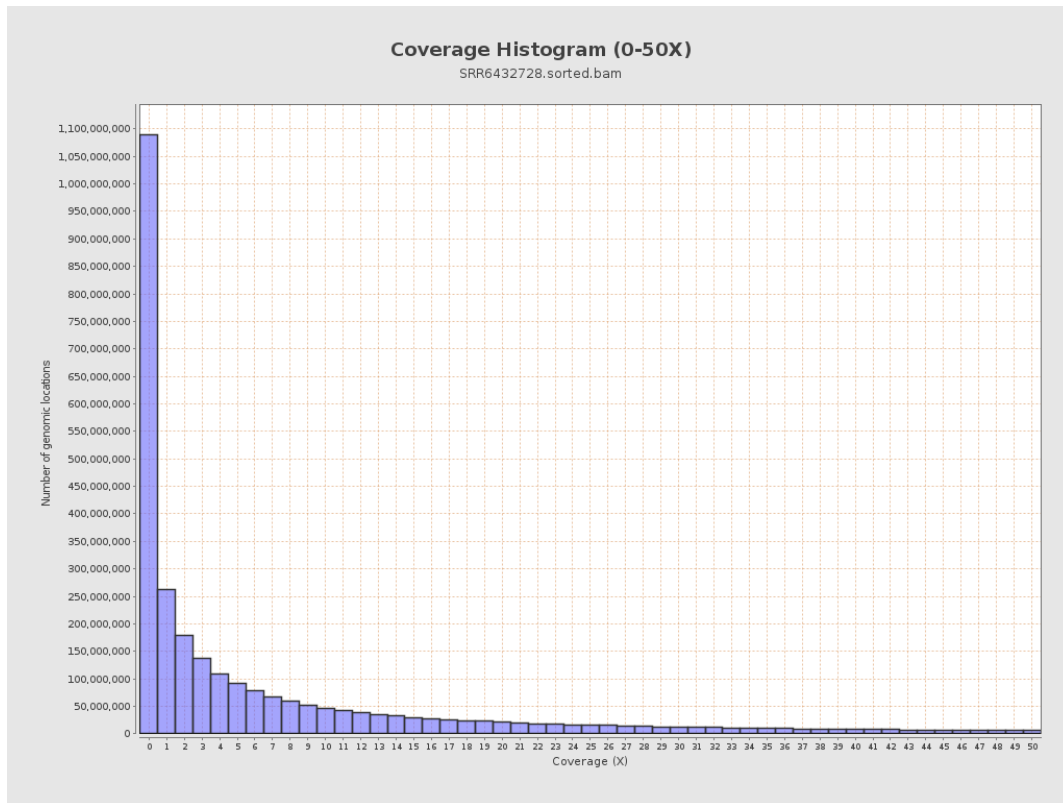
3. Results : Coverage across reference



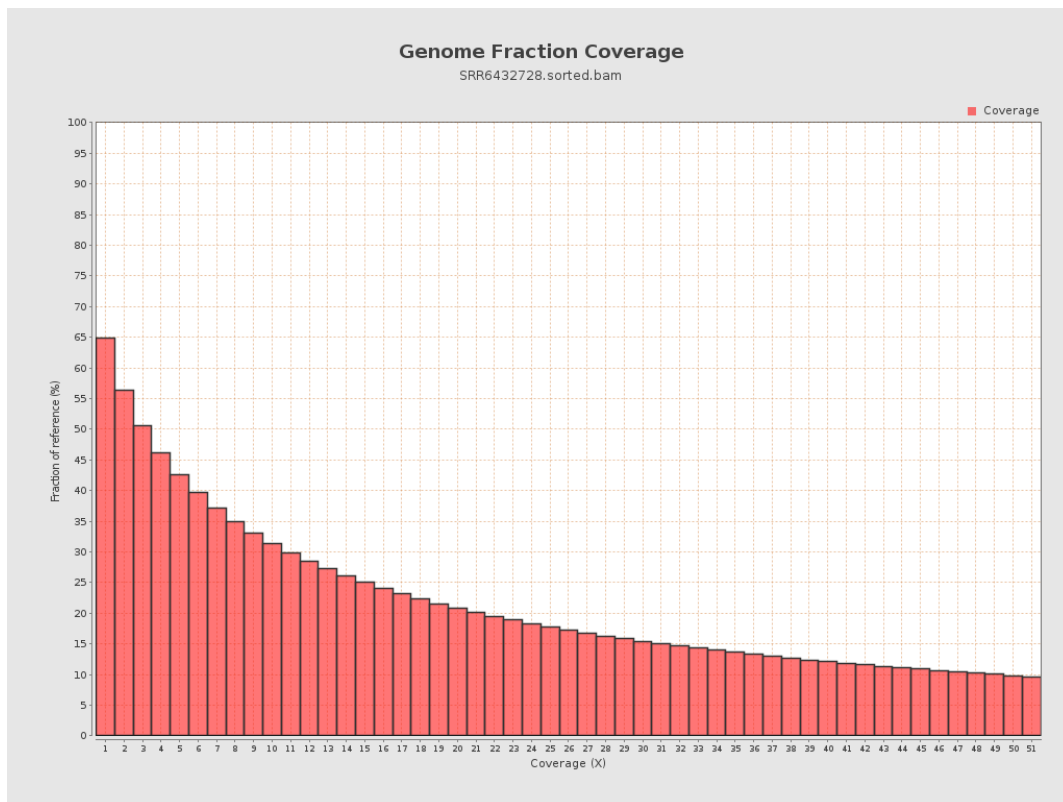
4. Results : Coverage Histogram



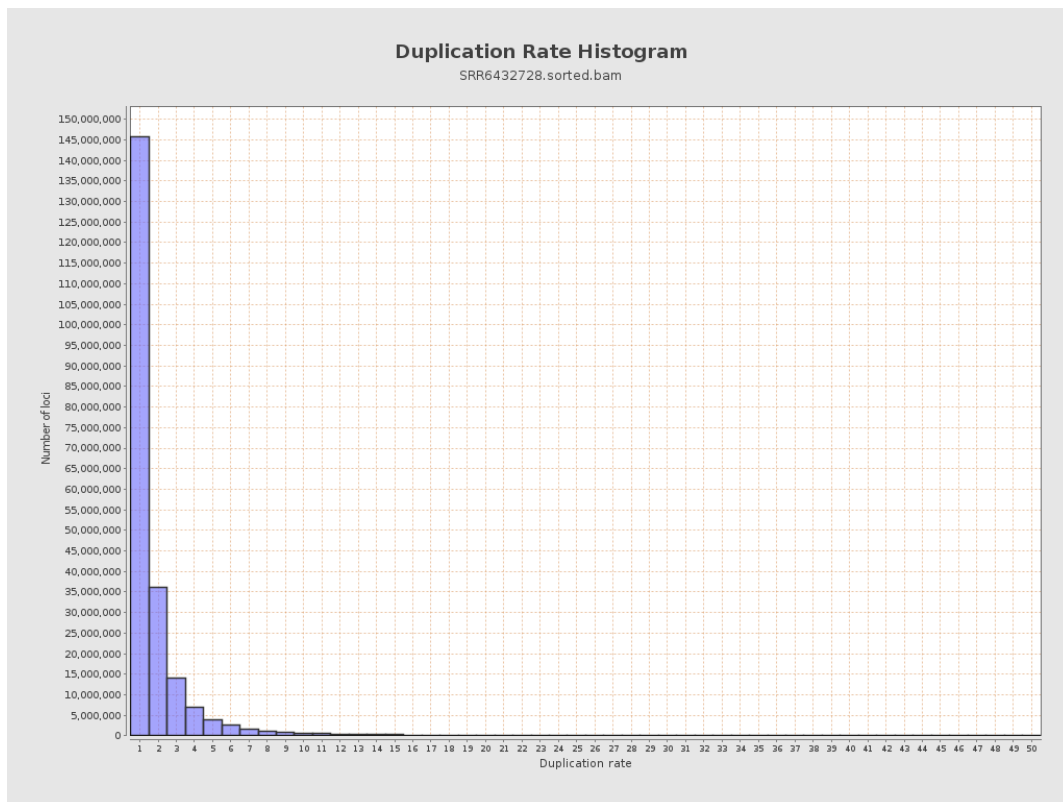
5. Results : Coverage Histogram (0-50X)



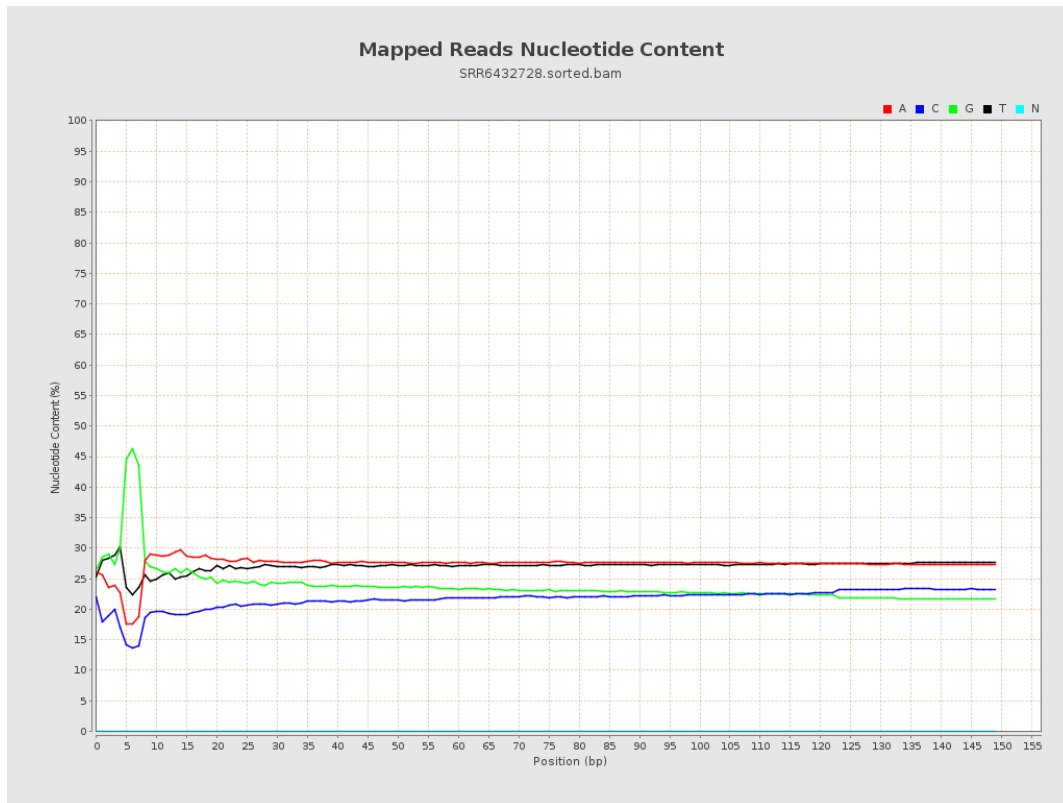
6. Results : Genome Fraction Coverage



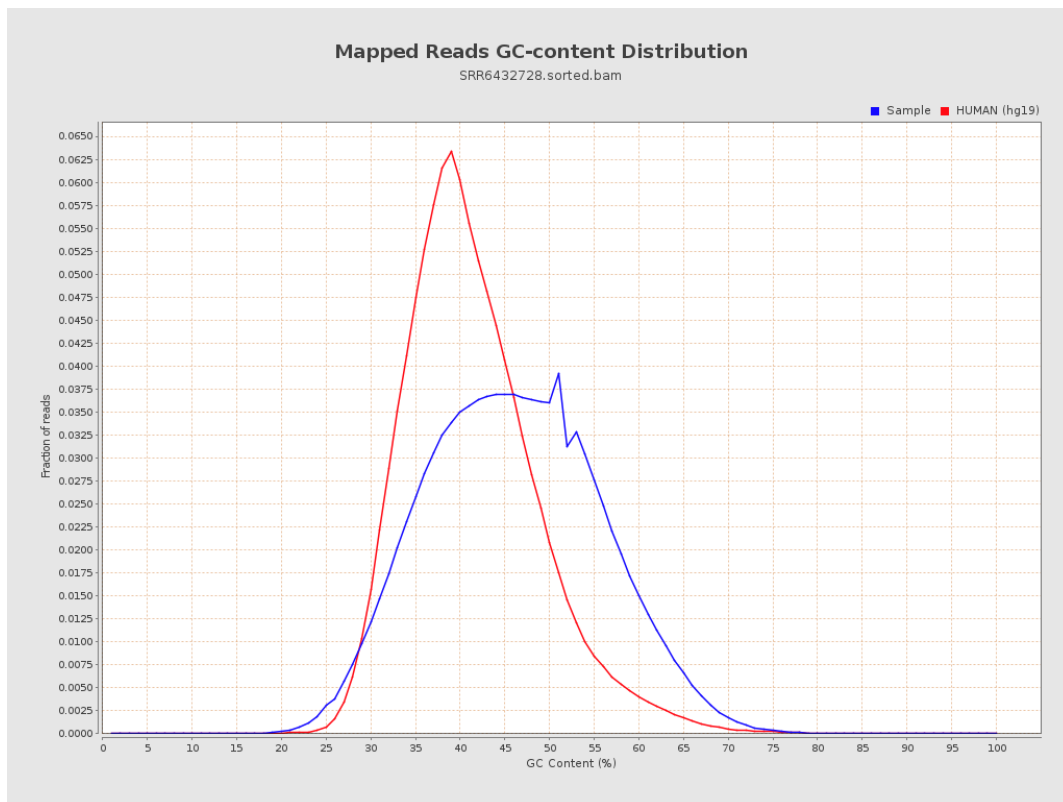
7. Results : Duplication Rate Histogram



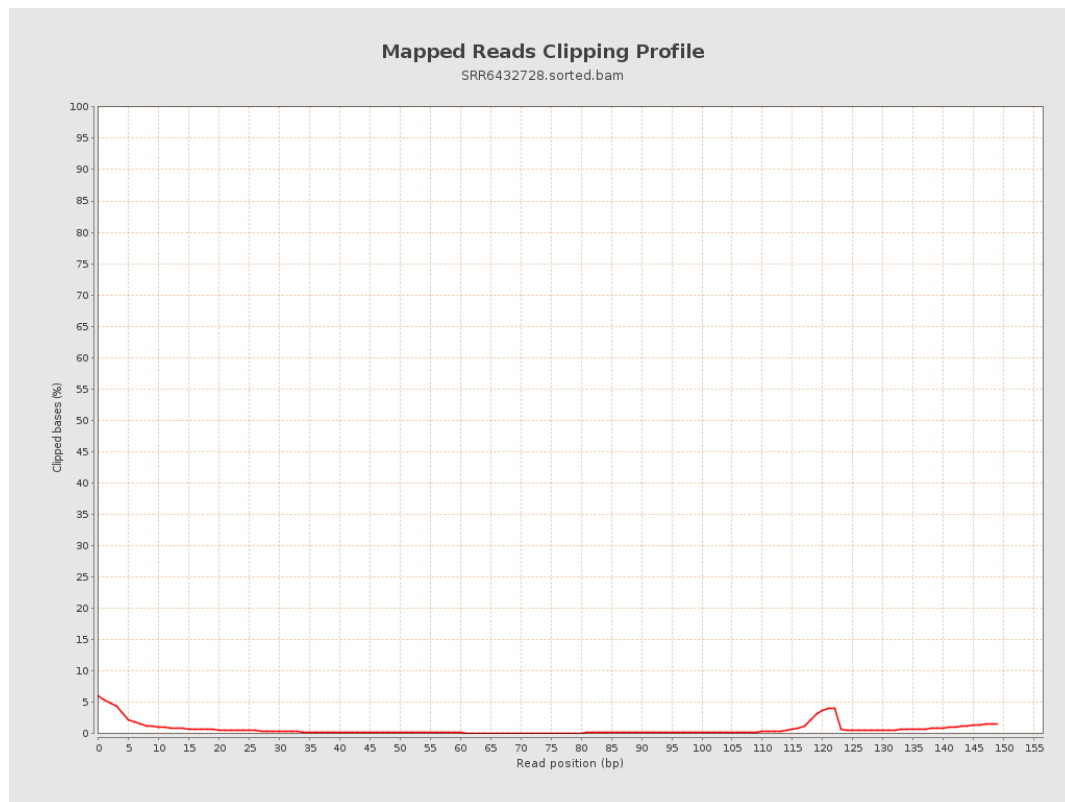
8. Results : Mapped Reads Nucleotide Content



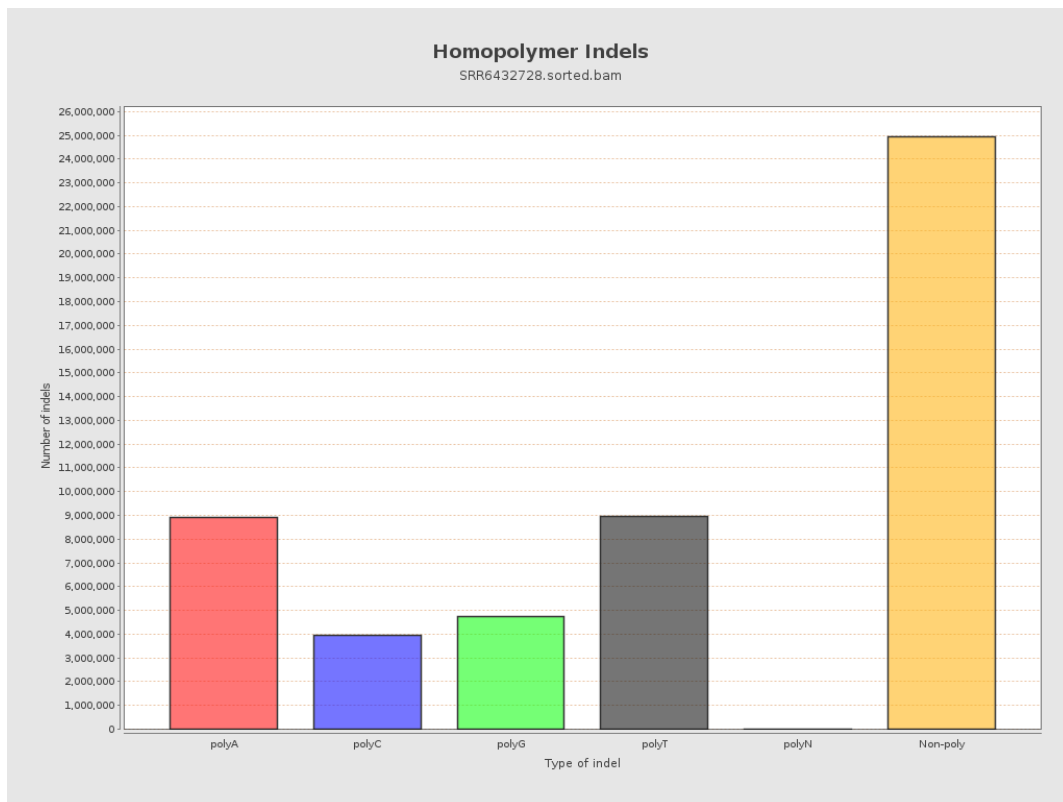
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



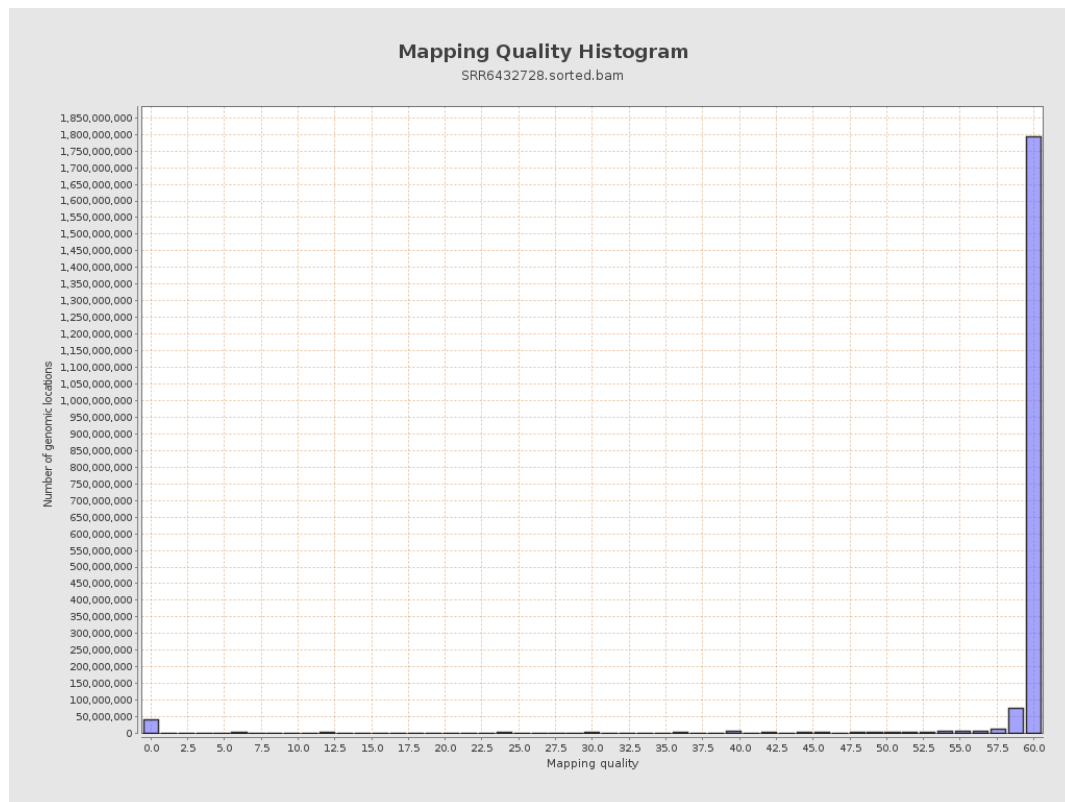
11. Results : Homopolymer Indels



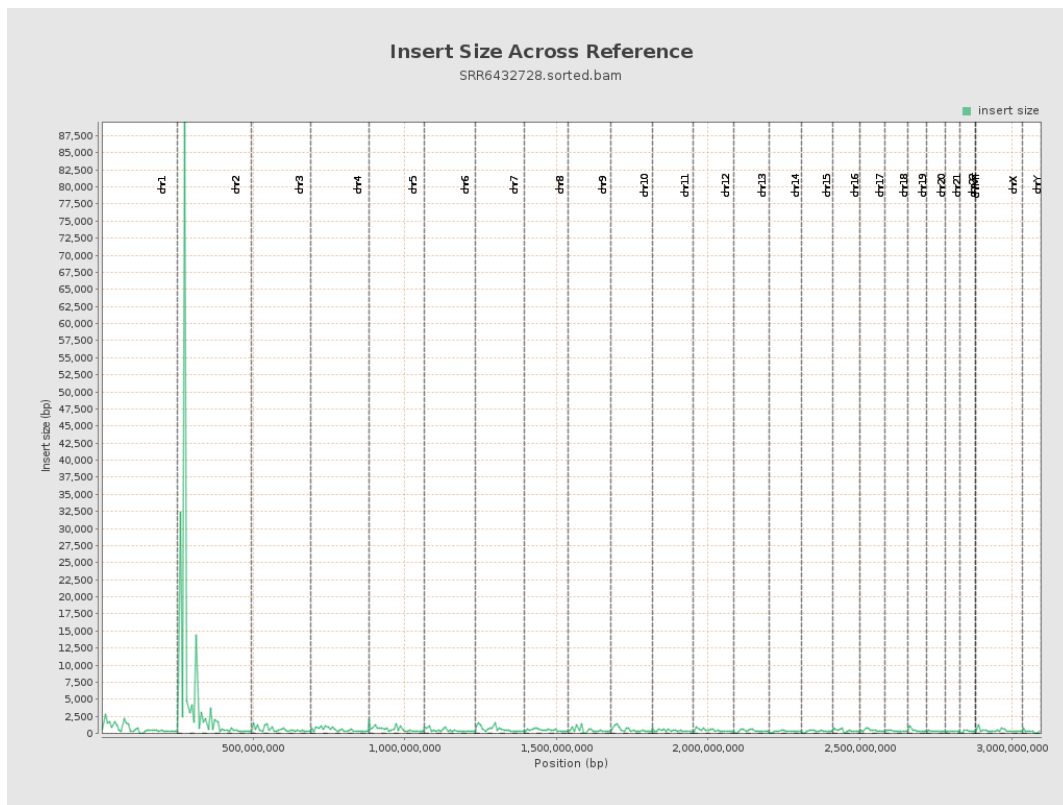
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

